

GenCore version 5.1.4\_p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:11:54 ; Search time 36808 Seconds  
(without alignments)  
1366.270 Million cell updates/sec

Title: US-09-920-394-3\_COPY\_14\_1741

Perfect score: 1728  
Sequence: 1 tgtgccttcacgatgtgg.....catagagctgtgaatgaaga 1728

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_em.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_or.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pi.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rpd.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	2.3	40	6	AX092543 Sequence
2	35.2	2.0	40	6	AX092544 Sequence
3	25	1.4	25	6	AX092545 Sequence
4	21.2	1.2	35	6	AR153460 Sequence
5	20.8	1.2	48	6	AX229460 Sequence
6	20.6	1.2	35	6	AR022645 Sequence
7	20.6	1.2	35	6	AR150983 Sequence
8	20.6	1.2	35	6	AR156053 Sequence
9	20.6	1.2	35	6	AX029519 Sequence
10	20.6	1.2	35	6	I87993 Sequence
11	20.6	1.2	47	6	AX194737 Sequence
12	20.4	1.2	32	6	A76878 Sequence
13	20.4	1.2	48	6	AX229366 Sequence
14	20.4	1.2	50	9	HUMKEREP8 L00204 Human K6b (
15	20.2	1.2	30	6	AR068140 Sequence
16	20.2	1.2	30	6	I31742 Sequence
17	20.2	1.2	30	6	I33417 Sequence
18	20.2	1.2	30	6	I38169 Sequence
19	20.2	1.2	30	6	I51133 Sequence
20	20.2	1.2	40	6	A05823 Sequence
21	20.2	1.2	43	9	HSU30421 A05823 Oligonucleo
22	20	1.2	31	6	AX463826 Sequence
23	19.6	1.1	50	9	HSJA7455 A7224655 Homo sapi
24	19.4	1.1	39	6	AR116809 Sequence
25	19.4	1.1	47	6	I68603 Sequence
26	19.4	1.1	48	6	E02389 DNA probe f
27	19.4	1.1	49	6	AX342584 Sequence
28	19.2	1.1	39	6	A93638 Sequence
29	19.2	1.1	39	6	AX023201 Sequence
30	19.2	1.1	40	10	MUSTRBRK I35090 Mus musculu
31	19.2	1.1	43	6	AR028659 Sequence
32	19.2	1.1	43	6	AR053752 Sequence
33	19.2	1.1	43	6	AR146252 Sequence
34	19.2	1.1	43	6	AR178206 Sequence
35	19.2	1.1	43	6	I73331 Sequence
36	19.2	1.1	48	6	AX426723 Sequence
37	19.2	1.1	49	6	A05822 A05822 Oligonucleo
38	19.2	1.1	49	6	AR009419 Sequence
39	19.2	1.1	49	6	AR009443 Sequence
40	19.2	1.1	49	6	AR009444 Sequence
41	19.2	1.1	49	6	AX167829 Sequence
42	19.2	1.1	49	6	AX167830 Sequence
43	19.2	1.1	49	6	I16524 Sequence
44	19.2	1.1	49	6	I16548 Sequence
45	19.2	1.1	49	6	I16549 Sequence

ALIGNMENTS

RESULT 1  
AX092543  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

AX092543 Sequence 4 from Patent WO0116358.  
AX092543  
AX092543.1 GI:13444635  
synthetic construct.  
synthetic construct  
artificial sequences  
1 (bases 1 to 40)  
Borg-Capra, C.S., Lehner, R.J. and Vance, D.E.  
Method of screening for triacylglycerol hydrolase inhibitors  
Patent: WO 0116358-A 4 08-MAR-2001;  
GLAXO GROUP LIMITED (GB) ; THE GOVERNORS OF THE UNIVERSITY OF

AX092543 linear DNA 40 bp PAT 21-MAR-2001

ALBERTA (CA)  
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Location/Qualifiers  
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/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligo"  
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Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 535 GCATCTGGGATCTTCACACAGGGGATGAACACAGCCG 574  
Db 1 GCATCTGGGATCTTCACACAGGGGATGAACACAGCCG 40  
RESULT 2  
AX092544/c  
LOCUS AX092544 40 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 5 from Patent WO0116358.  
ACCESSION AX092544  
VERSION AX092544.1 GI:13444636  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 40)  
AUTHORS Borg-Capra,C.S., Lehner,R.J. and Vance,D.E.  
TITLE Method of screening for triacylglycerol hydrolase inhibitors  
JOURNAL Patent: WO 0116358-A 5 08-MAR-2001;  
GLAXO GROUP LIMITED (GB) ; THE GOVERNORS OF THE UNIVERSITY OF ALBERTA (CA)  
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Location/Qualifiers  
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Best Local Similarity 92.5%; Pred. No. 95;  
Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1491 CTAGCAAGATGATGAATCTGGGCAACTTTGGCTC 1530  
Db 40 CTCAGCAAAATGATGAATCTGGGCAACTTTGGCTC 1  
RESULT 3  
AX092546/c  
LOCUS AX092546 25 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 7 from Patent WO0116358.  
ACCESSION AX092546  
VERSION AX092546.1 GI:13444638  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Borg-Capra,C.S., Lehner,R.J. and Vance,D.E.  
TITLE Method of screening for triacylglycerol hydrolase inhibitors  
JOURNAL Patent: WO 0116358-A 7 08-MAR-2001;  
GLAXO GROUP LIMITED (GB) ; THE GOVERNORS OF THE UNIVERSITY OF ALBERTA (CA)  
FEATURES  
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BASE COUNT 3 a 6 c 6 g 10 t

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Best Local Similarity 100.0%; Pred. No. 7.9e+04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1697 CCAGACAGAACACATAGAGCTGTGA 1721  
Db 25 CCAGACAGAACACATAGAGCTGTGA 1  
RESULT 4  
AR153460  
LOCUS AR153460 35 bp DNA linear PAT 08-AUG-2001  
DEFINITION Sequence 30 from patent US 6235515.  
ACCESSION AR153460  
VERSION AR153460.1 GI:15120992  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 35)  
AUTHORS Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A., Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.  
TITLE Malathion carboxylesterase  
JOURNAL Patent: US 6235515-A 30 22-MAY-2001;  
FEATURES  
source  
Location/Qualifiers  
1..35  
/organism="unknown"  
BASE COUNT 4 a 8 c 7 g 5 t 11 others  
ORIGIN  
Query Match 1.2%; Score 21.2; DB 6; Length 35;  
Best Local Similarity 60.0%; Pred. No. 1e+06;  
Matches 21; Conservative 4; Mismatches 10; Indels 0; Gaps 0;  
QY 165 TTCTGGGAATCCCTTTTGCACAGCCGCTCTTGG 199  
Db 1 TTCTGGGATNCCNTAYGCNMACCCNCCNTGG 35  
RESULT 5  
AX229460/c  
LOCUS AX229460 48 bp mRNA linear PAT 10-SEP-2001  
DEFINITION Sequence 2832 from Patent WO0157206.  
ACCESSION AX229460  
VERSION AX229460.1 GI:15558601  
KEYWORDS synthetic construct.  
SOURCE synthetic construct.  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 48)  
AUTHORS Fattaey,A.R., Jarvis,T., Meswiggen,J., Boohar,R.N. and Holman,P.S.  
TITLE Method and reagent for the inhibition of checkpoint kinase-1 (CHK 1) enzyme  
JOURNAL Patent: WO 0157206-A 2832 09-AUG-2001;  
RIBOZYME PHARMACEUTICALS, INC. (US) ; Fattaey, Ali R. (US)  
FEATURES  
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Location/Qualifiers  
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ORIGIN  
Query Match 1.2%; Score 20.8; DB 6; Length 48;  
Best Local Similarity 64.6%; Pred. No. 1.4e+06;  
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
QY 963 CAACCCCTTCTGGGCACTGTGATTTGATGGATGCTGCTGCTGAAACA 1010  
Db 48 CAACCCCTTCCCGACCATGCTCTTGAAGGAGTTCTCTCCGAAAAA 1

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BASE COUNT	5 a	6 c 7 g
ORIGIN		6 t 11 others
Query Match	1.2%	Score 20.6; DB 6; Length 35;
Best Local Similarity	61.3%;	Pred. No. 1.6e+06;
Matches	19; Conservative	6; Mismatches 6; Indels 0; Gaps 0;
QY 627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657		
DB 35 AAYATHGCVNMTTYGGNGRAYCCAAGCT 5		
RESULT 9		
AX029519/c		
LOCUS	AX029519	35 bp DNA linear PAT 16-SEP-2000
DEFINITION	Sequence 3 from Patent EP0981953.	
ACCESSION	AX029519	
VERSION	AX029519.1	GI:10190256
KEYWORDS	Exophiala spinifera.	
SOURCE	Exophiala spinifera.	
ORGANISM	Exophiala spinifera	
REFERENCE	1 (bases 1 to 35)	
AUTHORS	Duvick, J., Maddox, J.R., Rood, T.A. and Wang, X.	
TITLE	Transgenic plants transformed with fumonisin detoxifying enzymes	
JOURNAL	Patent: EP 0981953-A 3 01-MAR-2000;	
FEATURES	PIONEER HI BRED INT (US)	
source	Location/Qualifiers	
BASE COUNT	5 a	6 c 7 g
ORIGIN		6 t 11 others
Query Match	1.2%;	Score 20.6; DB 6; Length 35;
Best Local Similarity	61.3%;	Pred. No. 1.6e+06;
Matches	19; Conservative	6; Mismatches 6; Indels 0; Gaps 0;
QY 627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657		
DB 35 AAYATHGCVNMTTYGGNGRAYCCAAGCT 5		
RESULT 10		
I87993/c		
LOCUS	I87993	35 bp DNA linear PAT 10-AUG-1998
DEFINITION	Sequence 3 from patent US 5716820.	
ACCESSION	I87993	
VERSION	I87993.1	GI:3407933
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 35)	
AUTHORS	Duvick, J., Rood, T. and Wang, X.	
TITLE	Fumonisin detoxification enzymes	
JOURNAL	Patent: US 5716820-A 3 10-FEB-1998;	
FEATURES	Location/Qualifiers	
source	1. .35	
BASE COUNT	5 a	6 c 7 g
ORIGIN		6 t 11 others
Query Match	1.2%;	Score 20.6; DB 6; Length 35;
Best Local Similarity	61.3%;	Pred. No. 1.6e+06;
Matches	19; Conservative	6; Mismatches 6; Indels 0; Gaps 0;
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Db 48 AGATGTTGACTGTCCCAACGCCCTTCGCCCAATTCAGCCTCTGGAGAGG 3

## RESULT 15

AR068140/c AR068140 30 bp DNA linear PAT 29-SEP-1999

LOCUS AR068140 Sequence 6 from patent US 5852187.

DEFINITION AR068140

ACCESSION AR068140

VERSION AR068140.1 GI:5999362

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)

AUTHORS Thorner,M.O., Gaylinn,B.D., Horikawa,R. and Lyons,C.E. Jr.

TITLE Molecular cloning of the ovine pituitary growth hormone releasing hormone receptor

JOURNAL Patent: US 5852187-A 6 22-DEC-1998;

FEATURES Location/Qualifiers

source 1..30

BASE COUNT 7 a 10 c 10 g 3 t

ORIGIN

Query Match 1.2%; Score 20.2; DB 6; Length 30;

Best Local Similarity 88.0%; Pred. No. 2e+06;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 599 GGTGGCTGCCCTGCCTGGGTCCAG 623

Db 30 GGAGGCTGCCCTGAGCTGGTCCAG 6

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Search completed: May 21, 2003, 05:36:39

Job time : 36831 secs



GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:09:54 ; Search time 392 Seconds  
(without alignments)  
9927.176 Million cell updates/sec

Title: US-09-920-394-3\_COPY\_14\_1741

Perfect score: 1728

Sequence: 1 tgtgccttcacgatgtgg.....catagagctgtgaatgaaga 1738

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	2.3	40	22 AAF75811	Triacylglycerol hy
2	39	2.3	50	22 AAL33656	Human SNP oligonuc
3	35.2	2.0	40	22 AAF75812	Triacylglycerol hy
4	30	1.7	30	24 ABT04547	Human CES1 gene pr
5	25	1.4	25	22 AAF75814	Triacylglycerol hy
6	22.4	1.3	50	20 AAZ34198	Human PRO237 hybr
7	22.4	1.3	50	21 AAC78815	Human PRO237 hybr
8	22.4	1.3	50	21 AAC58128	Human PRO237 hybr
9	22.4	1.3	50	21 AAA88445	Antitumour PRO237

c	10	22.2	1.3	47	21	AAZ66351	Human map-related
c	11	22	1.3	22	24	ABT04612	Human CES1 gene pr
c	12	21.2	1.2	35	18	AAT68598	MA-alpha-E7 gene p
c	13	21.2	1.2	41	24	ABL52742	Nucleophosmin 9.68
c	14	21.2	1.2	21	24	ABL52743	Nucleophosmin 9.68
c	15	21	1.2	21	24	ABT04613	Human CES1 gene pr
c	16	20.8	1.2	40	21	AAA51139	Oligomer SLT-A Rev
c	17	20.8	1.2	48	22	AAH97618	Human Chk1 ribozym
c	18	20.6	1.2	35	17	AAT13972	E. spinifera fumon
c	19	20.6	1.2	35	20	AAH05722	E. spinifera fumon
c	20	20.6	1.2	47	21	AAZ87344	Human map-related
c	21	20.6	1.2	47	23	AAH88367	CNS disorder-relat
c	22	20.4	1.2	41	24	ABK15231	Geminivirus motion
c	23	20.4	1.2	48	22	AAH97524	Human Chk1 ribozym
c	24	20.2	1.2	29	19	AAV58768	Human secreted pro
c	25	20.2	1.2	30	15	AAQ45309	Human acromegalic
c	26	20.2	1.2	30	18	AAT47106	Human acromegalic
c	27	20.2	1.2	30	20	AAV81455	Probe #2 for human
c	28	20.2	1.2	44	21	AAZ55430	Neisseria species
c	29	20.2	1.2	49	22	AAH25471	5' PCR primer used
c	30	20	1.2	31	24	AAI47965	Recombinant porcin
c	31	20	1.2	45	20	AAZ27669	(SPPLn internal re
c	32	20	1.2	45	24	ABL51767	Hydroxyproline-ric
c	33	20	1.2	47	21	AAAG3889	Primer for cDNA en
c	34	20	1.2	50	21	AAC27036	Human secreted pro
c	35	19.8	1.1	42	18	AAT85655	Canine immunoglobi
c	36	19.6	1.1	48	24	ABN72300	Streptococcus agal
c	37	19.6	1.1	48	24	ABN72301	Streptococcus agal
c	38	19.6	1.1	50	21	AAH77273	Human clone c94398
c	39	19.4	1.1	34	12	AAQ14188	Probe NTL based on
c	40	19.4	1.1	40	19	AAV47799	Maize polymorphic
c	41	19.4	1.1	41	19	AAV51110	Maize polymorphic
c	42	19.4	1.1	47	16	AAT05673	Primer RD050 for 5
c	43	19.4	1.1	48	11	AAQ05100	Probe including si
c	44	19.4	1.1	49	24	ABA98751	Ribosome binding s
c	45	19.4	1.1	50	22	AAH25965	Rice genomic fragm

#### ALIGNMENTS

##### RESULT 1

AAF75811  
ID AAF75811 standard; DNA; 40 BP.

AC AAF75811;

XX AAF75811;

DT 16-MAY-2001 (first entry)

XX Triacylglycerol hydrolase, TGH, oligonucleotide P-TGHI.

XX TGH; triacylglycerol hydrolase; carboxylesterase; EST-1; VLDL; rat;

XX very low density lipoprotein; atherosclerosis; hypercholesterolaemia;

XX hyperbetaipoproteinaemia; non-insulin dependent diabetes mellitus;

XX coronary arterial disease; peripheral vascular disease; pancreatitis;

XX obesity; mixed dyslipidaemia; cerebro-vascular disease; mouse; pig; ss.

OS Mus sp.

OS Rattus sp.

OS Sus scrofa.

XX WO200116358-A2.

PN 08-MAR-2001.

PD 24-AUG-2000; 2000WO-EP08262.

XX 28-AUG-1999; 99GB-0020334.

XX (GLAXO) GLAXO GROUP LTD.

XX (UYAL-) UNIV ALBERTA.

XX Borg-Capra CS, Lehner RJ, Vance DE;





XX PS Disclosure; Page 10; 28pp; English.

CC The present invention relates to a method for identifying compounds

CC useful in the treatment of conditions resulting from elevated circulating

CC levels of: triglycerides, apoB-100, and/or very low density lipoproteins

CC (VLDL)/ low density lipoproteins (LDL)-cholesterol. The method comprises

CC determining whether the compound inhibits triacylglycerol hydrolase (TGH)

CC activity. TGH has previously been known as carboxylesterase EST-1. It is

CC thought that TGH may participate in the mobilisation of triacylglycerides

CC for assembly into VLDL. Inhibitors of TGH are useful for treating

CC atherosclerosis, hypercholesterolaemia, hyperbetalipoproteinaemia,

CC non-insulin dependent diabetes mellitus (NIDDM), coronary arterial

CC disease, peripheral vascular disease, pancreatitis, obesity, mixed

CC dyslipidaemia and cerebro-vascular disease. The present sequence is an

CC oligonucleotide which was used to clone human TGH (see AAB73263). The

CC present sequence was designed using conserved sites between mouse, rat

CC and pig TGH coding sequences.

XX Sequence 40 BP; 10 A; 9 C; 9 G; 12 T; 0 other;

Qy Query Match 2.0%; Score 35.2; DB 22; Length 40;

Db Best Local Similarity 92.5%; Pred. No. 0.83;

Matches 37; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1491 CTTAGCAAGATGGTGATGAATCTGGGCCAACTTTGCTC 1530

Db 40 CTCAGCAAAATGGTGATGAATCTGGGCCAACTTTGCTC 1

RESULT 4

ABT04547

ID ABT04547 standard; DNA; 30 BP.

AC ABT04547;

DT 25-SEP-2002 (first entry)

DE Human CES1 gene probe SEQ ID NO: 13.

XX Human; drug metabolism; enzyme; probe; ss.

OS Homo sapiens.

XX JP2002142780-A.

XX 21-MAY-2002.

XX 28-AUG-2001; 2001JP-0257338.

XX 04-SEP-2000; 2000JP-0267163.

XX (SAKA ) OTSUKA SEIYAKU KOGYO KK.

XX WPI; 2002-552472/59.

XX Measurement of an enzyme participating to the first phase reaction of

PT drug metabolism, a probe and a kit for it

XX Claim 4; Page 18; 36pp; Japanese.

XX The present invention relates to probes which can be used for the

CC measurement-of an enzyme. The probes can be used for the measurement of

CC an enzyme participating to the first phase reaction of drug metabolism.

CC The present sequence is a probe shown in the invention.

XX Sequence 30 BP; 9 A; 7 C; 7 G; 7 T; 0 other;

Qy Query Match 1.7%; Score 30; DB 24; Length 30;

Best Local Similarity 100.0%; Pred. No. 29;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 993 ATGCTGCTGCTGAACACCTGAAGAGCTT 1022

Db 1 ATGCTGCTGCTGAACACCTGAAGAGCTT 30

RESULT 5

AAF75814/c

ID AAF75814 standard; DNA; 25 BP.

XX AAF75814;

DT 16-MAY-2001 (first entry)

XX Triacylglycerol hydrolase, TGH, oligonucleotide hCE3 Rev.

XX TGH; triacylglycerol hydrolase; carboxylesterase; EST-1; VLDL;

XX very low density lipoprotein; atherosclerosis; hypercholesterolaemia;

XX hyperbetalipoproteinaemia; non-insulin dependent diabetes mellitus;

XX coronary arterial disease; peripheral vascular disease; pancreatitis;

XX obesity; mixed dyslipidaemia; cerebro-vascular disease; human; ss.

OS Homo sapiens.

XX WO200116358-A2.

XX 08-MAR-2001.

XX 24-AUG-2000; 2000WO-EP08262.

XX 28-AUG-1999; 99GB-0020334.

XX (GLAX ) GLAXO GROUP LTD.

XX (UYAL-) UNIV ALBERTA.

XX Borg-Capra CS, Lehner RJ, Vance DE;

XX WPI; 2001-235119/24.

XX Identifying compounds for treating elevated circulating levels of

PT triglyceride, very low density lipoprotein/low density

PT lipoprotein-cholesterol and apoB-100, comprises identifying

PT triacylglycerol hydrolase inhibitors

XX Disclosure; Page 11; 28pp; English.

XX The present invention relates to a method for identifying compounds

CC useful in the treatment of conditions resulting from elevated circulating

CC levels of: triglycerides, apoB-100, and/or very low density lipoproteins

CC (VLDL)/ low density lipoproteins (LDL)-cholesterol. The method comprises

CC determining whether the compound inhibits triacylglycerol hydrolase (TGH)

CC activity. TGH has previously been known as carboxylesterase EST-1. It is

CC thought that TGH may participate in the mobilisation of triacylglycerides

CC for assembly into VLDL. Inhibitors of TGH are useful for treating

CC atherosclerosis, hypercholesterolaemia, hyperbetalipoproteinaemia,

CC non-insulin dependent diabetes mellitus (NIDDM), coronary arterial

CC disease, peripheral vascular disease, pancreatitis, obesity, mixed

CC dyslipidaemia and cerebro-vascular disease. The present sequence is an

CC oligonucleotide which was used to clone human TGH (see AAB73263). The

CC present sequence corresponds to the 3' end of human carboxylesterase I

CC (hCEI).

XX Sequence 25 BP; 3 A; 6 C; 6 G; 10 T; 0 other;

Qy Query Match 1.4%; Score 25; DB 22; Length 25;

Best Local Similarity 100.0%; Pred. No. 9.3e+02;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1697 CCAGACAGAACACATAGAGCTGTGA 1721

Db 25 CCAGACAGAACACATAGAGCTGTGA 1

RESULT 6

AA234198/c



AAC7815/c  
ID AAC78815 standard; DNA; 50 BP.  
XX AC AAC78815;  
XX DT  
XX DE 08-FEB-2001 (first entry)  
XX DE Human PRO237 hybridisation probe SEQ ID NO:361.  
XX KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;  
XX KW expressed sequence tag; detection; cancer; PCR primer; probe; ss.  
XX OS  
XX XX Homo sapiens.  
XX PN WO200053756-A2.  
XX PD 14-SEP-2000.  
XX PF 18-FEB-2000; 2000WO-US04341.  
XX PR 08-MAR-1999; 99WO-US05028.  
XX PR 12-MAR-1999; 99US-0123957.  
XX PR 29-MAR-1999; 99US-0126773.  
XX PR 21-APR-1999; 99US-0130232.  
XX PR 28-APR-1999; 99US-0131445.  
XX PR 14-MAY-1999; 99US-0134287.  
XX PR 23-JUN-1999; 99US-0141037.  
XX PR 26-JUL-1999; 99US-0145698.  
XX PR 29-OCT-1999; 99US-0162506.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 02-DEC-1999; 99WO-US28551.  
XX PR 16-DEC-1999; 99WO-US30095.  
XX PR 30-DEC-1999; 99WO-US31243.  
XX PR 30-DEC-1999; 99WO-US31274.  
XX PR 05-JAN-2000; 2000WO-US00219.  
XX PR 06-JAN-2000; 2000WO-US00277.  
XX PR 06-JAN-2000; 2000WO-US00376.  
XX PA (GETH ) GENENTECH INC.  
XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX PI Ferrara N, Flivaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;  
XX PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;  
XX PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;  
XX PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;  
XX DR WPI: 2000-611443/58.  
XX XX  
XX PT Novel PRO polypeptides and polynucleotides used in detection methods,  
XX PT to target bioactive molecules to specific cells, and to modulate  
XX PT cellular activities -  
XX PS  
XX PS Example 55; Page 285; 636pp; English.  
XX CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed  
XX CC sequence tag) sequences which encode secreted or transmembrane PRO  
XX CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic  
XX CC activity. The polynucleotides and polypeptides can be used for detecting  
XX CC the presence of PRO polypeptides in samples, for linking bioactive  
XX CC molecules to cells and for modulating biological activities of cells,  
XX CC using the polypeptides for specific targeting. The polypeptide targeting  
XX CC can be used to kill the target cells, e.g. for the treatment of cancers.  
XX CC The polypeptide pairs provide specific targeting of bioactive molecules  
XX CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in  
XX CC the isolation of the PRO polynucleotide sequences.  
XX SQ Sequence 50 BP; 8 A; 20 C; 7 G; 15 T; 0 other;  
Query Match 1.3%; Score 22.4; DB 21; Length 50;  
Best Local Similarity 66.7%; Pred. No. 9.1e+03;  
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1209 GAAGCCACTGAGAATACTAGGAGGAACAGACGACACTGTCAAAAAG 1256  
||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||  
Db 50 GAGCGGACTGAGGAATGGTTAGAGGTACTGGCAACGTTGACAAGAG 3  
RESULT 8  
AAC58128/c  
ID AAC58128 standard; DNA; 50 BP.  
XX AC AAC58128;  
XX DT  
XX DE 25-JAN-2001 (first entry)  
XX DE Human PRO237 hybridisation probe SEQ ID NO:39.  
XX KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;  
XX KW tumorigenesis; detection; neoplastic cell growth; proliferation;  
XX KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;  
XX KW immunological disorder; hybridisation; probe; PCR primer; ss.  
XX OS  
XX XX Homo sapiens.  
XX PN WO200053754-A1.  
XX XX 14-SEP-2000.  
XX XX 06-JAN-2000; 2000WO-US00277.  
XX PR 08-MAR-1999; 99WO-US05028.  
XX PR 12-MAR-1999; 99US-0123957.  
XX PR 29-MAR-1999; 99US-0126773.  
XX PR 21-APR-1999; 99US-0130232.  
XX PR 28-APR-1999; 99US-0131445.  
XX PR 05-OCT-1999; 99WO-US23089.  
XX PR 30-NOV-1999; 99WO-US28313.  
XX PR 02-DEC-1999; 99WO-US28551.  
XX PR 16-DEC-1999; 99WO-US28564.  
XX PR 30-DEC-1999; 99WO-US31243.  
XX PR 30-DEC-1999; 99WO-US31274.  
XX PA (GETH ) GENENTECH INC.  
XX PI Baker KP, Desauvage FJ, Goddard A, Gurney AL, Klein RD, Roy MA;  
XX PI Wood WI;  
XX DR WPI: 2000-572269/53.  
XX XX  
XX PT New isolated antibody for use in compositions and methods for the  
XX PT diagnosis and treatment of neoplastic cell growth and proliferation in  
XX PT mammals, including humans, and in monitoring tumor treatment -  
XX PS  
XX PS Example 2; Page 95; 195pp; English.  
XX CC The present invention describes an isolated antibody (Ab) that binds to  
XX CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,  
XX CC PRO237, PRO324, PRO351, PRO362, PRO615, PRO531, PRO3664, PRO618,  
XX CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions  
XX CC and methods for the diagnosis and treatment of neoplastic cell growth  
XX CC and proliferation in mammals, including humans. Genes and polypeptides  
XX CC encoded by them, that are amplified in the genome of a tumour cell, can  
XX CC be identified and are useful targets for the treatment and prevention of  
XX CC certain cancers and may be used to monitor tumour treatment. Compounds  
XX CC that inhibit the expression or activity of the identified polypeptides  
XX CC can be identified and used as antagonists. Benign or malignant tumours,  
XX CC inflammatory disorders and immunological disorders can be treated.  
XX CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used  
XX CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and  
XX CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein  
XX CC sequences given in the exemplification of the present invention.  
XX SQ Sequence 50 BP; 8 A; 20 C; 7 G; 15 T; 0 other;  
Query Match 1.3%; Score 22.4; DB 21; Length 50;

1

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XX Human; drug metabolism; enzyme; probe; ss.
KW OS Homo sapiens.
XX JP2002142780-A.
XX PD 21-MAY-2002.
XX PF 28-AUG-2001; 2001JP-0257338.
XX PR 04-SEP-2000; 2000JP-0267163.
XX PA (SAKA ) OTSUKA SEIYAKU KOGYO KK.
XX DR WPI; 2002-552472/59.
XX PT Measurement of an enzyme participating to the first phase reaction of
PT drug metabolism, a probe and a kit for it
XX PS Claim 8; Page 26; 36pp; Japanese.
XX CC The present invention relates to probes which can be used for the
CC measurement of an enzyme. The probes can be used for the measurement of
CC an enzyme participating to the first phase reaction of drug metabolism.
CC The present sequence is a probe shown in the invention.
XX SQ Sequence 22 BP; 6 A; 8 C; 4 G; 4 T; 0 other;

Query Match 1.3%; Score 22; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 952 CCAGAGAGATCAACCCCTTCT 973
DB 1 CCAGAGAGATCAACCCCTTCT 22

RESULT 12
AAT68598
ID AAT68598 standard; DNA; 35 BP.
XX AC AAT68598;
XX DT 08-AUG-1997 (first entry)
XX DE Md-alpha-E7 gene primer Mdl.
XX KW Malathion carboxylesterase; organophosphate; insecticide;
KW pesticide; remediation; bioremediation; decontamination;
KW Musca domestica; polymerase chain reaction; PCR; primer; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 9
FT /*tag= a
FT /*mod_base= i
FT modified_base 12
FT /*tag= b
FT /*mod_base= i
FT modified_base 15
FT /*tag= c
FT /*mod_base= i
FT modified_base 21
FT /*tag= d
FT /*mod_base= i
FT modified_base 27
FT /*tag= e
FT /*mod_base= i
FT modified_base 30
FT /*tag= f
FT /*mod_base= i

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XX WO9719176-A1.
XX PD 29-MAY-1997;
XX PF 22-NOV-1996; 96WO-AU00746.
XX PR 23-NOV-1995; 95AU-0006751.
XX PA (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX PI Boyce T, Brownlie JC, Campbell PM, Claudianos C;
PI Newcomb RD, Oakeshott JG, Robin GC, Russell RJ, Smyth K;
XX DR WPI; 1997-298113/27.
XX PT DNA encoding enzyme that degrades organophosphate pesticides -
PT useful for decontamination of soil, water, food etc
XX PS Disclosure; Page 14; 52pp; English.
XX CC Consensus generic alpha-esterase primers (AAT68598-99) were designed
CC to the conserved regions of multiple amino acid alignments of
CC Drosophila melanogaster and Lucilia cuprina alpha-esterase
CC genes (see also AAT68596), and used in a PCR amplification of
CC Musca domestica genomic DNA. Primer Mdl corresponds to residues
CC 58-69 of L. cuprina alpha-E7 and Md2 to nucleotides 92-83. A 540
CC bp amplicon was used to screen a M. domestica genomic library to
CC isolate the Md alpha-E7 gene (AAT68597).
XX SQ Sequence 35 BP; 4 A; 8 C; 7 G; 5 T; 11 other;

Query Match 1.2%; Score 21.2; DB 18; Length 35;
Best Local Similarity 60.0%; Pred. No. 1.7e+04;
Matches 21; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 165 TTCCTGGGAATCCCTTTGCCAAGCCGCTCTTGG 199
DB 1 TTCGAGGGNATNCNTAYGCNARCNCNCBNTGG 35

RESULT 13
ABL52742/c
ID ABL52742 standard; DNA; 41 BP.
XX AC ABL52742;
XX DT 01-JUL-2002 (first entry)
XX DE Nucleophosmin 9.68 associated probe 1.
XX KW Nucleophosmin 9.68; cytostatic; virucidal; immunomodulatory;
KW antinflammatory; haemostatic; malignant tumour; haemopathy; HIV;
KW immunological disease; inflammatory disease; probe; ss.
XX OS Unidentified.
XX PN WO200206471-A1.
XX PD 24-JAN-2002.
XX PF 29-JUN-2001; 2001WO-CN01074.
XX PR 30-JUN-2000; 2000CN-0116971.
XX PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX PI Mao Y, Xie Y;
XX DR WPI; 2002-122632/16.
XX PT Nucleophosmin 9.68 polynucleotide and polypeptide, useful in diagnosis
PT and treatment of malignant tumour, haemopathy, HIV infection,

```

PT Immunological diseases and various inflammatory diseases -

XX .PS Example 6; Page 21; 36pp; Chinese.

XX CC The invention relates to an isolated nucleophosmin 9.68 polypeptide.  
CC CC The activity of the protein of the invention may be described as,  
CC CC cytostatic, virucidal, immunomodulatory, antiinflammatory and  
CC CC haemostatic. The polypeptide and encoded polynucleotide are applicable in  
CC CC diagnosis and treatment of malignant tumour, haemopathy, HIV infection,  
CC CC immunological diseases and various inflammatory diseases. The screened  
CC CC compounds as well as their preparations are also useful for treating  
CC CC the diseases mentioned above. The current sequence represents a  
XX CC nucleophosmin 9.68 associated probe.

SQ Sequence 41 BP; 8 A; 10 C; 13 G; 10 T; 0 other;

Query Match 1.2%; Score 21.2; DB 24; Length 41;  
Best Local Similarity 88.5%; Pred. No. 1.9e+04;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 565 AACACAGCCGGGGAACTGGGGTCAC 590  
||||||| ||||||| |||||  
Db 41 AACACAGCCGTGGAACTGGGGTCAC 16

RESULT 14

ABL52743/C  
ID ABL52743 standard; DNA; 41 BP.

XX AC ABL52743;

XX DT 01-JUL-2002 (first entry)

XX DE Nucleophosmin 9.68 associated probe 2.

XX KW Nucleophosmin 9.68; cytostatic; virucidal; immunomodulatory;  
XX KW antiinflammatory; haemostatic; malignant tumour; haemopathy; HIV;  
XX KW immunological disease; inflammatory disease; probe; ss.

XX OS Unidentified.

XX PN WO200206471-A1.

XX PD 24-JAN-2002.

XX PF 29-JUN-2001; 2001WO-CN01074.

XX PR 30-JUN-2000; 2000CN-0116971.

XX PA (SHAN-) SHANGHAI BIOWIND GENE DEV INC.

XX PI Mao Y, Xie Y;

XX PI WPI; 2002-122632/16.

XX PT Nucleophosmin 9.68 polynucleotide and polypeptide, useful in diagnosis  
XX PT and treatment of malignant tumour, haemopathy, HIV infection,  
XX PT immunological diseases and various inflammatory diseases -

XX PS Example 6; Page 21; 36pp; Chinese.

XX CC The invention relates to an isolated nucleophosmin 9.68 polypeptide.  
XX CC The activity of the protein of the invention may be described as,  
XX CC cytostatic, virucidal, immunomodulatory, antiinflammatory and  
XX CC haemostatic. The polypeptide and encoded polynucleotide are applicable in  
XX CC diagnosis and treatment of malignant tumour, haemopathy, HIV infection,  
XX CC immunological diseases and various inflammatory diseases. The screened  
XX CC compounds as well as their preparations are also useful for treating  
XX CC the diseases mentioned above. The current sequence represents a  
XX CC nucleophosmin 9.68 associated probe.

SQ Sequence 41 BP; 8 A; 10 C; 13 G; 10 T; 0 other;

Query Match 1.2%; Score 21.2; DB 24; Length 41;  
Best Local Similarity 88.5%; Pred. No. 1.9e+04;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 565 AACACAGCCGGGGAACTGGGGTCAC 590  
||||||| ||||||| |||||  
Db 41 AACACAGCCGTGGAACTGGGGTCAC 16

RESULT 15

ABT04613/C  
ID ABT04613 standard; DNA; 21 BP.

XX AC ABT04613;

XX DT 25-SEP-2002 (first entry)

XX DE Human CES1 gene probe SEQ ID NO: 79.

XX KW Human; drug metabolism; enzyme; probe; ss.

XX OS Homo sapiens.

XX PN JP2002142780-A.

XX PD 21-MAY-2002.

XX PF 28-AUG-2001; 2001JP-0257338.

XX PR 04-SEP-2000; 2000JP-0267163.

XX PA (SAKA ) OTSUKA SEIYAKU KOGYO KK.

XX DR WPI; 2002-552472/59.

XX PT Measurement of an enzyme participating to the first phase reaction of  
XX PT drug metabolism, a probe and a kit for it

XX PS Claim 8; Page 26; 36pp; Japanese.

XX CC The present invention relates to probes which can be used for the  
XX CC measurement of an enzyme. The probes can be used for the measurement of  
XX CC an enzyme participating to the first phase reaction of drug metabolism.  
XX CC The present sequence is a probe shown in the invention.

SQ Sequence 21 BP; 3 A; 7 C; 3 G; 8 T; 0 other;

Query Match 1.2%; Score 21; DB 24; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1058 GGTCGGAATTACACAGCAGGA 1078  
||||||| ||||||| |||||  
Db 21 GGTCGGAATTACACAGCAGGA 1

Search completed: May 20, 2003, 19:22:37  
Job time : 395 secs

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:14:44 ; Search time 87 Seconds  
(without alignments)  
6091.235 Million cell updates/sec

Title: US-09-920-394-3\_COPY\_14\_1741

Perfect score: 1728

Sequence: 1 tgcgcctccagctggtg.....catagagctggaatgaaga 1728

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PTCUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.2	1.2	35	4	US-09-068-960-30
2	20.6	1.2	35	1	US-08-805-814-3
3	20.6	1.2	35	1	US-08-484-815-3
4	20.6	1.2	35	3	US-08-888-949-3
5	20.6	1.2	35	4	US-08-888-950-3
6	20.6	1.2	35	4	US-09-282-758-3
7	20.6	1.2	35	5	PCT-US95-10284-3
8	20.2	1.2	30	1	US-08-073-799C-6
9	20.2	1.2	30	1	US-07-946-232-6
10	20.2	1.2	30	1	US-07-947-672-6
11	20.2	1.2	30	1	US-08-432-043-6
12	20.2	1.2	30	2	US-08-660-963-6
13	20.2	1.2	47	3	US-09-284-737-8
14	19.4	1.1	39	3	US-08-907-598-4
15	19.4	1.1	47	1	US-08-426-020-3
16	19.2	1.1	43	1	US-07-988-194A-25
17	19.2	1.1	43	1	US-08-258-152-27
18	19.2	1.1	43	2	US-08-076-299A-27
19	19.2	1.1	43	2	US-08-438-582-27
20	19.2	1.1	43	4	US-09-266-596-27
21	19.2	1.1	43	4	US-08-479-737-25
22	19.2	1.1	43	4	US-08-475-442A-25
23	19.2	1.1	49	1	US-08-258-188-3
24	19.2	1.1	49	1	US-08-258-188-28
25	19.2	1.1	49	1	US-08-258-188-29
26	19.2	1.1	49	1	US-08-526-813-3
27	19.2	1.1	49	1	US-08-526-813-28

28	19.2	1.1	49	1	US-08-526-813-29
29	19.2	1.1	49	5	PCT-US95-08554-3
30	19.2	1.1	49	5	PCT-US95-08554-28
31	19.2	1.1	49	5	PCT-US95-08554-29
32	19	1.1	36	1	US-08-805-814-4
33	19	1.1	36	1	US-08-484-815-4
34	19	1.1	36	3	US-08-888-949-4
35	19	1.1	36	4	US-08-888-950-4
36	19	1.1	36	4	US-09-262-758-4
37	19	1.1	36	5	PCT-US95-10284-4
38	19	1.1	47	3	US-08-726-807B-21
39	19	1.1	47	3	US-09-258-367-21
40	19	1.1	47	4	US-09-546-550-21
41	19	1.1	47	4	US-09-431-414-21
42	19	1.1	47	4	US-09-225-670-21
43	19	1.1	47	4	US-09-431-349C-21
44	19	1.1	49	1	US-08-484-493-4
45	19	1.1	49	1	US-08-484-494-4

#### ALIGNMENTS

#### RESULT 1

US-09-068-960-30

; Sequence 30, Application US/09068960A

; Patent No. 6235515

; GENERAL INFORMATION:

; APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.

; TITLE OF INVENTION: MALATHION CARBOXYLESTERASE

; FILE REFERENCE: Attorney Docket No. 6235515 50179-051

; CURRENT APPLICATION NUMBER: US/09/068,960A

; CURRENT FILING DATE: 1998-05-20

; EARLIER APPLICATION NUMBER: PCT/AU96/00746

; EARLIER FILING DATE: 1996-11-22

; EARLIER APPLICATION NUMBER: AU 6751

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 30

; LENGTH: 35

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Degenerate

; OTHER INFORMATION: Primer

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (9)

; OTHER INFORMATION: 1

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (12)

; OTHER INFORMATION: 1

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (15)

; OTHER INFORMATION: 1

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (21)

; OTHER INFORMATION: 1

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (27)

; OTHER INFORMATION: 1

; FEATURE:

; NAME/KEY: modified\_base

; LOCATION: (30)

; OTHER INFORMATION: 1

; US-09-068-960-30

Query Match

1.2%; Score 21.2; DB 4; Length 35;

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Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 21; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

-QY 165 TTCTGGGAATCCCTTTTCCAGCCGCCCTCTTGG 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 TTCGAGGNATNCNTAYGCNMRCCNCBNTGG 35

- RESULT 2
US-08-805-814-3/C
; Sequence 3, Application US/08805814
; Patent No. 5716820
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Rood, Tracy A.
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: FUMONISIN DETOXIFICATION
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: IA
; COUNTRY: USA
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Windows 3.1 - No. 5716820epad
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,814
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Roth, Michael J.
; REGISTRATION NUMBER: 29,342
; REFERENCE/DOCKET NUMBER: 0272 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515-248-4895
; TELEFAX: 515-248-4934
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 bases
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: probe
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-805-814-3

Query Match 1.2%; Score 20.6; DB 1; Length 35;
Best Local Similarity 61.3%; Pred. No. 3.7e+03;
Matches 19; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

-QY 627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
      ||:||||: ||:||||: ||:||||: ||:||||:
Db 35 AAYATHGCVNMTTYGGNGNRAYCCAAGCT 5

- RESULT 3
US-08-484-815-3/C
; Sequence 3, Application US/08484815
; Patent No. 5792931
; GENERAL INFORMATION:
; APPLICANT: DUVICK, JONATHAN
; APPLICANT: ROOD, TRACY A.
; TITLE OF INVENTION: FUMONISIN DETOXIFICATION COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Pioneer Hi-Bred International
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,815
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Bobrowicz, Donna I.
; REGISTRATION NUMBER: 32,196
; REFERENCE/DOCKET NUMBER: 0272 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515 248-4895
; TELEFAX: 515 248-4934
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-484-815-3

Query Match 1.2%; Score 20.6; DB 1; Length 35;
Best Local Similarity 61.3%; Pred. No. 3.7e+03;
Matches 19; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

-QY 627 AACATTGCCAGCTTTGGAGGGAACCCAGGCT 657
      ||:||||: ||:||||: ||:||||: ||:||||:
Db 35 AAYATHGCVNMTTYGGNGNRAYCCAAGCT 5

- RESULT 4
US-08-888-949-3/C
; Sequence 3, Application US/08888949
; Patent No. 6025188
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan
; APPLICANT: Maddox, Joyce R.
; APPLICANT: Rood, Tracy A.
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: FUMONISIN DETOXIFICATION COMPOSITIONS
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
; STREET: Darwin Building, 7100 N.W. 62nd Ave., P.O.
; STREET: Box 1000
; CITY: Johnston
; STATE: Iowa
; COUNTRY: USA
; ZIP: 50131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,949
; FILING DATE: 07-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rood, Tracy A.
; REGISTRATION NUMBER: 32,196
; REFERENCE/DOCKET NUMBER: 0272 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 515 248-4895
; TELEFAX: 515 248-4934
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-888-949-3/C
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TYPE: nucleic acid  
STRANDEDNESS: single

Db 35 AAYATHGCNVMNTTYGGNGGNRAYCCAAGCT 5

## RESULT 7

PCT-US95-10284-3/c  
; Sequence 3, Application PC/TUS9510284

; GENERAL INFORMATION:

; APPLICANT: PIONEER HI-BRED INTERNATIONAL, INC.

; TITLE OF INVENTION: FUMONISIN DETOXIFICATION COMPOSITIONS

; TITLE OF INVENTION: AND METHODS

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pioneer Hi-Bred International

; STREET: 700 Capital Square, 400 Locust Street

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: U.S.A.

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/10284

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bobrowicz, Donna I.

; REGISTRATION NUMBER: 32,196

; REFERENCE/DOCKET NUMBER: 0272-PCT

; TELEPHONE: 515 248-4895

; TELEFAX: 515 248-4844

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 35 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US95-10284-3

## Query Match

Best Local Similarity 1.2%; Score 20.6; DB 5; Length 35;

Matches 19; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

## QY 627

AACATGCGCAGCTTGGAGGGAACCCAGGCT 657

||||| : ||||| : ||||| : |||||

DB 35 AAYATGCGNMTTGGNGNRAYCCAAGCT 5

## RESULT 8

US-08-073-799C-6/c

; Sequence 6, Application US/08073799C

; Patent No. 5583010

; GENERAL INFORMATION:

; APPLICANT: Zysk, John R.

; APPLICANT: Baumbach, William R.

; APPLICANT: Thorne, Michael O.

; APPLICANT: Gaylinn, Bruce D.

; APPLICANT: Lynch, Kevin R.

; APPLICANT: Harrison, Jeffrey K.

; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND

; TITLE OF INVENTION: PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING HORMONE REC

; TITLE OF INVENTION: AND CLONING OF A GENE ENCODING FOR THE GROWTH HORMONE RELEASIN

; TITLE OF INVENTION: HORMONE RECEPTOR

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.

; STREET: Metropolitan Square Building, Suite 800, 1450 G St., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/073,799C

FILING DATE: June 10, 1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/902,826

FILING DATE: 23-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: O'Shaughnessy, Brian P.

REGISTRATION NUMBER: 32,747

REFERENCE/DOCKET NUMBER: 1574/81-2216

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-824-8000

TELEFAX: 202-824-8199

TELEX: 248516

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-073-799C-6

Query Match 1.2%; Score 20.2; DB 1; Length 30;

Best Local Similarity 88.0%; Pred. No. 4.5e+03;

Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## QY 599

GGTGGCTGCCCTCGCTGGGTCCAG 623

||||| : |||||| : |||||

DB 30 GGAGGCTGCCCTGAGTGGTCCAG 6

## RESULT 9

US-07-946-232-6/c

; Sequence 6, Application US/07946232

; Patent No. 5591641

; GENERAL INFORMATION:

; APPLICANT: Thorne, Michael O.

; APPLICANT: Gaylinn, Bruce D.

; APPLICANT: Lynch, Kevin R.

; APPLICANT: Harrison, Jeffrey K.

; APPLICANT: Zysk, John R.

; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND

; TITLE OF INVENTION: PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING

; TITLE OF INVENTION: HORMONE RECEPTOR AND CLONING OF A GENE ENCODING FOR THE

; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MASON, FENWICK & LAWRENCE

; STREET: 1225 I Street, N.W., Suite 1000

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/946,232

FILING DATE: 19920915

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/902,826

FILING DATE: 23-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Schein, Daniel B.

REGISTRATION NUMBER: 33,551

REFERENCE/DOCKET NUMBER: 1084/81-1317  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-289-1200  
TELEFAX: 202-289-6674  
TELEX: 248516  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-07-946-232-6

Query Match 1.2%; Score 20.2; DB 1; Length 30;  
Best Local Similarity 88.0%; Pred. No. 4.5e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 599 GGTGGTCCCTGGCTGGGTCCAG 623  
Db 30 GGAGGCTGCCCTGAGCTGGCTCCAG 6

## RESULT 10

US-07-947-672-6/c  
Sequence 6, Application US/07947672  
Patent No. 5612470  
GENERAL INFORMATION:  
APPLICANT: Thorne, Michael O.  
APPLICANT: Gaylinn, Bruce D.  
APPLICANT: Lynch, Kevin R.  
APPLICANT: Harrison, Jeffrey K.  
APPLICANT: Zysk, John R.  
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND  
TITLE OF INVENTION: PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING  
TITLE OF INVENTION: HORMONE RECEPTOR AND CLONING OF A GENE ENCODING FOR THE  
TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MASON, FENWICK & LAWRENCE  
STREET: 1225 I Street, N.W., Suite 1000  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/07/947,672  
APPLICATION NUMBER: 19920918  
FILING DATE: 23-JUN-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 07/902,826  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Schein, Daniel B.  
REGISTRATION NUMBER: 33,551  
REFERENCE/DOCKET NUMBER: 1084/81-1365  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-289-1200  
TELEFAX: 202-289-6674  
TELEX: 248516  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-07-947-672-6

Query Match 1.2%; Score 20.2; DB 1; Length 30;  
Best Local Similarity 88.0%; Pred. No. 4.5e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 599 GGTGGTCCCTGGCTGGGTCCAG 623  
Db 30 GGAGGCTGCCCTGAGCTGGCTCCAG 6

## RESULT 11

US-08-432-043-6/c  
Sequence 6, Application US/08432043  
Patent No. 5644046  
GENERAL INFORMATION:  
APPLICANT: Thorne, Michael O.  
APPLICANT: Gaylinn, Bruce D.  
APPLICANT: Lynch, Kevin R.  
APPLICANT: Harrison, Jeffrey K.  
APPLICANT: Zysk, John R.  
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND  
TITLE OF INVENTION: PROTEIN SEQUENCING OF THE GROWTH HORMONE RELEASING  
TITLE OF INVENTION: HORMONE RECEPTOR AND CLONING OF A GENE ENCODING FOR THE  
TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: POPHAM HAIK SCHNOBRICH & KAUFMAN, LTD.  
STREET: 655 15th Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/432,043  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US 07/947,672  
FILING DATE: 18-SEP-1992  
APPLICATION NUMBER: US 07/902,826  
FILING DATE: 23-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: O'Shaughnessy, Brian P.  
REGISTRATION NUMBER: 32,747  
REFERENCE/DOCKET NUMBER: 18046.033  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-824-8000  
TELEFAX: 202-824-8199  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-432-043-6

Query Match 1.2%; Score 20.2; DB 1; Length 30;  
Best Local Similarity 88.0%; Pred. No. 4.5e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 599 GGTGGTCCCTGGCTGGGTCCAG 623  
Db 30 GGAGGCTGCCCTGAGCTGGCTCCAG 6

## RESULT 12

US-08-660-963-6/c

; Sequence 6, Application US/08660963  
; Patent No. 5852187  
; GENERAL INFORMATION:  
; APPLICANT: Thorner, Michael O.  
; APPLICANT: Gaylinn, Bruce D.  
; APPLICANT: Horikawa, Reiko  
; APPLICANT: Lyons Jr., Charles E.  
; TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY  
; TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECEPTOR  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: POPHAM, HAIK, SCHNOBRICH & KAUFMAN, LTD.  
; STREET: Metropolitan Square Building, Suite 800, 1450  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 12-JUN-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: O'Shaughnessy, Brian P.  
; REGISTRATION NUMBER: 32,747  
; REFERENCE/DOCKET NUMBER: 18046.036  
; TELEPHONE: 202-824-8000  
; TELEFAX: 202-824-8199  
; TELEX: 248516  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-660-963-6  
Query Match 1.2%; Score 20.2; DB 2; Length 30;  
Best Local Similarity 88.0%; Pred. No. 4.5e+03;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 599 GGTGGTGCCTGGCTGGCTGGCTGAG 623  
DB 30 GGAGGCTGCCCTGAGCTGCTCCAG 6  
RESULT 13  
US-09-264-737-8/c  
; Sequence 8, Application US/09264737A  
; Patent No. 6107549  
; GENERAL INFORMATION:  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Ruff, Thomas G.  
; TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via  
; TITLE OF INVENTION: Expression of Esterase Enzymes  
; FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance  
; CURRENT APPLICATION NUMBER: US/09/264,737A  
; CURRENT FILING DATE: 1999-03-09  
; EARLIER APPLICATION NUMBER: 60/077,377  
; EARLIER FILING DATE: 1998-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: thermal amplification sequence homologous to RLE3  
; OTHER INFORMATION: divergent region flanking sequence  
US-09-264-737-8  
Query Match 1.2%; Score 20; DB 3; Length 47;  
Best Local Similarity 65.9%; Pred. No. 6.8e+03;  
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 522 CAATATCGCTGGCATCTGGGATCTTCACACACAGGGGATCA 565  
DB 47 CAGTACCGCTGGCATCTGGCTTCGTTTCAACATCGATCA 4  
RESULT 14  
US-08-907-598-4/c  
; Sequence 4, Application US/08907598  
; Patent No. 6139833  
; GENERAL INFORMATION:  
; APPLICANT: Burgess, Rob  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur  
; TITLE OF INVENTION: TARGETED GENE DISCOVERY  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/907,598  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 8535-015-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 493-4935  
; TELEFAX: (650) 493-5556  
; TELEX: 66141  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 39 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ANTI-SENSE: NO  
; US-08-907-598-4  
Query Match 1.1%; Score 19.4; DB 3; Length 39;  
Best Local Similarity 70.3%; Pred. No. 9.3e+03;  
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 695 TGTCTCTGTTCTGTTTCTCTCCATTCGCCAAGAAC 731  
DB 39 TGTGTGAGTTCCTGTTCTGACTCATTTGTGTGATGAAC 3  
RESULT 15  
US-08-426-020-3/c  
; Sequence 3, Application US/08426020  
; Patent No. 5676952

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; GENERAL INFORMATION:
; APPLICANT: AUDONNET, JEAN-CHRISTOPHE F
; APPLICANT: DARTHEIL, RAPHAEL J
; APPLICANT: RIVIERE, MICHEL A
; APPLICANT: ZELNIK, VLADIMIR
; APPLICANT: ROSS, LOUIS J
; TITLE OF INVENTION: HERPESVIRUSES TRANSFORMED TO EXPRESS gD
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LARSON AND TAYLOR
; STREET: 727 SOUTH 23RD STREET
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,020
; FILING DATE: 09-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SARRO, THOMAS P
; REGISTRATION NUMBER: 19,396
; REFERENCE/DOCKET NUMBER: XI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-920-7200
; TELEFAX: 703-892-8428
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-426-020-3

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Query Match      1.1%; Score 19.4; DB 1; Length 47;
Best Local Similarity 70.3%; Pred. No. 1e+04;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1594 ATCTGCAGATTGGTCCCAACACCCAGCGGCCGAGAA 1630
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Db 44 ATCTCGAAGTGGTGACAAATATCATCGCGCGCGGAA 8

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Search completed: May 21, 2003, 06:16:16  
Job time : 90 secs



GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:16:04 ; Search time 900 Seconds  
(without alignments)

2535.288 Million cell updates/sec

Title: US-09-920-394-3\_COPY\_14\_1741

Perfect score: 1728

Sequence: 1 tgcgccttcacgatgtgg.....catagagctgtgaatgaaga 1728

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Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 650231138 residues

Total number of hits satisfying chosen parameters: 504518

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	22.4	1.3	50	9	US-09-978-295A-361
C 2	22.4	1.3	50	9	US-09-978-697-361
C 3	22.4	1.3	50	9	US-09-978-192A-361
C 4	22.4	1.3	50	9	US-09-999-832A-361
C 5	22.4	1.3	50	9	US-09-978-189-361
C 6	22.4	1.3	50	9	US-09-978-608A-361
C 7	22.4	1.3	50	9	US-09-978-191A-361
C 8	22.4	1.3	50	9	US-09-978-403A-361
C 9	22.4	1.3	50	9	US-09-978-564A-361
C 10	22.4	1.3	50	9	US-09-978-585A-361
C 11	22.4	1.3	50	9	US-10-017-081A-361
C 12	22.4	1.3	50	9	US-09-978-824-361
C 13	22.4	1.3	50	9	US-09-981-915A-361
C 14	22.4	1.3	50	9	US-09-999-833A-361
C 15	22.4	1.3	50	9	US-10-167-749-361
C 16	22.4	1.3	50	9	US-09-918-585A-361
C 17	22.4	1.3	50	9	US-09-978-423A-361
C 18	22.4	1.3	50	9	US-10-013-921A-361
C 19	22.4	1.3	50	9	US-09-978-193A-361

C 20	22.4	1.3	50	9	US-10-013-929A-361
C 21	22.4	1.3	50	9	US-10-016-177A-361
C 22	22.4	1.3	50	9	US-09-999-830A-361
C 23	22.4	1.3	50	9	US-09-978-757A-361
C 24	20.8	1.2	48	9	US-09-848-754A-8208
C 25	20.8	1.2	48	9	US-09-776-474-2832
C 26	20.6	1.2	35	10	US-09-731-393-3
C 27	20.4	1.2	48	9	US-09-776-474-2738
C 28	20.2	1.2	46	9	US-10-121-258-49
C 29	20.2	1.2	46	9	US-10-121-258-50
C 30	19.8	1.1	48	9	US-09-848-754A-8518
C 31	19.4	1.1	33	8	US-08-834-666A-26
C 32	19.4	1.1	33	8	US-08-834-666A-29
C 33	19.4	1.1	48	9	US-09-877-478-5309
C 34	19.4	1.1	48	9	US-09-848-754A-8732
C 35	19.2	1.1	25	10	US-09-866-108-4102
C 36	19.2	1.1	25	10	US-09-866-108-4103
C 37	19.2	1.1	31	9	US-09-773-599-4
C 38	19.2	1.1	31	9	US-09-773-599-18
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C 40	19.2	1.1	43	10	US-09-759-352-25
C 41	19	1.1	36	10	US-09-731-393-4
C 42	19	1.1	47	8	US-08-961-888-39
C 43	19	1.1	48	9	US-09-780-164-2417
C 44	18.8	1.1	39	9	US-10-067-443-31
C 45	18.8	1.1	48	9	US-09-780-164-2488

#### ALIGNMENTS

#### RESULT 1

US-09-978-295A-361/c  
; Sequence 361, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P630P1C11  
; CURRENT APPLICATION NUMBER: US/09/978,295A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249

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Sequence 361, App  
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Sequence 4102, Ap  
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Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
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## RESULT 4

US-09-999-832A-361/C  
; Sequence 361, Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC63  
; CURRENT APPLICATION NUMBER: US/09/999,832A  
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; PRIOR APPLICATION NUMBER: 09/918585  
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; PRIOR FILING DATE: 1997-10-17  
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25	PRIOR APPLICATION NUMBER: 60/084637
26	PRIOR FILING DATE: 1998-05-07
27	PRIOR APPLICATION NUMBER: 60/084639
28	PRIOR FILING DATE: 1998-05-07
29	PRIOR APPLICATION NUMBER: 60/084640
30	PRIOR FILING DATE: 1998-05-07
31	PRIOR APPLICATION NUMBER: 60/084598
32	PRIOR FILING DATE: 1998-05-07
33	PRIOR APPLICATION NUMBER: 60/084600
34	PRIOR FILING DATE: 1998-5-07
35	PRIOR APPLICATION NUMBER: 60/084627
36	PRIOR FILING DATE: 1998-05-07
37	PRIOR APPLICATION NUMBER: 60/084643
38	PRIOR FILING DATE: 1998-05-07
39	PRIOR APPLICATION NUMBER: 60/085339
40	PRIOR FILING DATE: 1998-05-13
41	PRIOR APPLICATION NUMBER: 60/085338
42	PRIOR FILING DATE: 1998-05-13
43	PRIOR APPLICATION NUMBER: 60/085323
44	PRIOR FILING DATE: 1998-05-13
45	PRIOR APPLICATION NUMBER: 60/085582
46	PRIOR FILING DATE: 1998-05-15
47	PRIOR APPLICATION NUMBER: 60/085700
48	PRIOR FILING DATE: 1998-05-15
49	PRIOR APPLICATION NUMBER: 60/085689
50	PRIOR FILING DATE: 1998-05-15
51	PRIOR APPLICATION NUMBER: 60/085579
52	PRIOR FILING DATE: 1998-05-15
53	PRIOR APPLICATION NUMBER: 60/085580
54	PRIOR FILING DATE: 1998-05-15
55	PRIOR APPLICATION NUMBER: 60/085573
56	PRIOR FILING DATE: 1998-05-15
57	PRIOR APPLICATION NUMBER: 60/085704
58	PRIOR FILING DATE: 1998-05-15
59	PRIOR APPLICATION NUMBER: 60/085697
60	PRIOR FILING DATE: 1998-05-15

RESULT 6  
US-09-978-608A-361/c  
; Sequence 361, Application US/09978608A  
; Publication No. US20030045462A1

Query Match	Best Local Similarity	Score	DB 9;	Length	50;
Matches 32;	Conservative 0;	Mismatches 16;	Indels 0;	Gaps 0;	
QY 1209	GAAGCCACTGAGAAATACCTAGAGAAACAGAGGACACTGTCAAAAG	1256			
DB 50	GAGGCGACTGAGGAATGGGTGAGGTACTGGCAAGCTTGACAAAGAG	3			
RESULT 7					
US-09-978-191A-361/c					
Sequence 361, Application US/09978191A					
Publication NO. US20030050239A1					
GENERAL INFORMATION:					
APPLICANT: Ashkenazi, Avi					
APPLICANT: Baker Kevin P.					
APPLICANT: Botstein, David					
APPLICANT: Desnoyers, Luc					
APPLICANT: Eaton, Dan					
APPLICANT: Ferrara, Napoleon					
APPLICANT: Filvaroff, Ellen					
APPLICANT: Fong, Sherman					
APPLICANT: Gao, Wei-Qiang					
APPLICANT: Gerber, Hanspeter					
APPLICANT: Gerritsen, Mary E.					
APPLICANT: Goddard, Audrey					
APPLICANT: Godowski, Paul J.					
APPLICANT: Grimaldi, J. Christopher					
APPLICANT: Gurney, Austin L.					
APPLICANT: Hillan, Kenneth J.					
APPLICANT: Kijavlin, Ivar J.					
APPLICANT: Kuo, Sophia S.					
APPLICANT: Napier, Mary A.					
APPLICANT: Pan, James					
APPLICANT: Paoni, Nicholas F.					
APPLICANT: Roy, Margaret Ann					
APPLICANT: Shelton, David L.					
APPLICANT: Stewart, Timothy A.					
APPLICANT: Tumas, Daniel					
APPLICANT: Williams, P. Mickey					
APPLICANT: Wood, William I.					
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic					
FILE REFERENCE: P2630P1C22					
CURRENT APPLICATION NUMBER: US/09/978,608A					
CURRENT FILING DATE: 2001-10-16					
NUMBER OF SEQ ID NOS: 624					
Prior Application removed - See File Wrapper or Palm					
SEQ ID NO 361					
LENGTH: 50					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Synthetic oligonucleotide probe					
US-09-978-608A-361					

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; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
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; PRIOR APPLICATION NUMBER: 60/083322  
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; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
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; PRIOR FILING DATE: 1998-05-06

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; PRIOR FILING DATE: 1998-05-07  
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; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;  
Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1209 GAAGCCACTGAGAAATACCTTAGGAGGACAGACAGACACTGTCAAAAAG 1256  
DB 50 GAGGCGACTGAGGATGGTGGTACTGAGGAGTGGCAAGCTTGACAAAGAG 3

RESULT 8  
US-09-978-403A-361/c  
; Sequence 361, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavini, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.



APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PLC17  
CURRENT APPLICATION NUMBER: US/09/978,403A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
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PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084639  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084640  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598

;/ PRIOR FILING DATE: 1998-05-07  
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;/ PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9; Length 50;

Best Local Similarity 56.7%; Pred. No. 2.5e+03;  
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1209 GAAGCCACTGAGAAATACCTTAGGAGGACAGACACACTGTCAAAAG 1256

Db 50 GAGCGACTGAGGATGGGTAGAGGTACTGGCACTGCACAAAG 3

## RESULT 9

US-09-978-564A-361/c  
; Sequence 361, Application US/09978564A  
; Publication No. US20030050241A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tomas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC25

;/ CURRENT APPLICATION NUMBER: US/09/978,564A  
;/ CURRENT FILING DATE: 2001-10-16  
;/ PRIOR FILING DATE: 1998-05-07  
;/ PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-04-08  
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; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
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; PRIOR FILING DATE: 1998-04-29  
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; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
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; PRIOR FILING DATE: 1998-05-05  
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; PRIOR APPLICATION NUMBER: 60/084640  
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; PRIOR APPLICATION NUMBER: 60/085573  
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; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3% Score 22.4; DB 9; Length 50;  
Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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RESULT 10

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; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C15  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 361  
; LENGTH: 50  
; TYPE: DNA





APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gunney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P630FIC12  
CURRENT APPLICATION NUMBER: US/09/981.915A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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PRIOR FILING DATE: 1998-04-29  
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Query Match 1.3%; Score 22.4; DB 9; Length 50;

Best Local Similarity 66.7%; Pred. No. 2.5e-03;

Matches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1209 GAAGCCACTGAGAAATACTTAGGAGGACAGACGACACTGTCAAAAAG 1256

Db 50 GAGGCGACTGAGATGGTGTAGAGTACTGGCAGCGTTGACAAAG 3

## RESULT 14

US-09-999-833A-361/c

; Sequence 361, Application us/0999833A

; Publication No. US20030054405A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC65  
; CURRENT APPLICATION NUMBER: US/09/999,833A  
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7	PRIOR APPLICATION NUMBER: 60/084414
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7	PRIOR APPLICATION NUMBER: 60/084640
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7	PRIOR APPLICATION NUMBER: 60/085579
7	PRIOR FILING DATE: 1998-05-15
7	PRIOR APPLICATION NUMBER: 60/085580
7	PRIOR FILING DATE: 1998-05-15
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7	PRIOR FILING DATE: 1998-05-15
7	PRIOR APPLICATION NUMBER: 60/085704
7	PRIOR FILING DATE: 1998-05-15
7	PRIOR APPLICATION NUMBER: 60/085697

Query Match 1.3%; Score 22.4; DB 9;  
Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
Matches 32; Conservative 0; Mismatches 16; Indels

**QY**      1209 GAAGCCACTGAGAAATACCTTAGGGGAACAGACGACACTGTCAAAAAG 1256  
          || || ||||||| ||| - |||| | | | | | | | | | |  
**Db**      50 GAGGCAGCTGAGGAATGGGTTAGAGTACTGGCAACGTTGACAAGAAG 3

RESULT 15  
US-10-167-749-361/c  
Sequence 361, Application US/10167749  
Publication No. US20030056137A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
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APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.



Search completed: May 21, 2003, 06:31:28  
Job time : 902 secs



GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: May 20, 2003, 19:12:59 ; Search time 2271 seconds  
(without alignments)  
12323.118 Million cell updates/sec

Title: US-09-920-394-3\_COPY\_14\_1741

Perfect score: 1728

Sequence: 1 tgcgccttcacgatgtgg.....catagagctgtgaatgaaga 1728

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*\*

1: em\_estba:\*\*

2: em\_esthum:\*\*

3: em\_estin:\*\*

4: em\_estnu:\*\*

5: em\_estov:\*\*

6: em\_estpl:\*\*

7: em\_estro:\*\*

8: em\_htc:\*\*

9: gb\_estl:\*\*

10: gb\_est2:\*\*

11: gb\_htc:\*\*

12: gb\_est3:\*\*

13: gb\_est4:\*\*

14: gb\_est5:\*\*

15: em\_estfun:\*\*

16: em\_estom:\*\*

17: gb\_gss:\*\*

18: em\_gss\_hum:\*\*

19: em\_gss\_inv:\*\*

20: em\_gss\_pin:\*\*

21: em\_gss\_vrt:\*\*

22: em\_gss\_fun:\*\*

23: em\_gss\_mam:\*\*

24: em\_gss\_mus:\*\*

25: em\_gss\_other:\*\*

26: em\_gss\_pro:\*\*

27: em\_gss\_rod:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	1.3	43	9	AA472672 vho4g03.r
2	20.8	1.2	50	17	AZ386495
3	20.6	1.2	50	17	AZ785734
4	20.4	1.2	49	9	A1348359
5	20.2	1.2	36	17	AZ491747
6	20.2	1.2	43	17	AZ391814

## RESULT 1

AA472672

LOCUS

DEFINITION

VH04G03.r1 Soares\_mammary\_gland\_NbMMG Mus musculus CDNA clone

IMAGE:874516 5', similar to SW:NDPM\_BOVIN P42029 NADH-UBIQUINONE

OXIDOREDUCTASE 19 KD SUBUNIT ;, mRNA sequence.

AA472672

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

## TITLE

JOURNAL

COMMENT

AA627247 9 AA627247 20.2 1.2 49 9 AA627247  
AW246898 10 AW246898 20 1.2 49 10 AW246898  
AU105489 9 AU105489 20 1.2 50 9 AU105489  
AU105492 9 AU105492 20 1.2 50 9 AU105492  
AU106827 11 50 9 AU106827 19.8 1.1 50 9 AU106827  
AU106827 12 50 9 AU106827 19.6 1.1 49 9 AU106827  
AA894674 13 50 9 AA894674 19.6 1.1 49 9 AA894674  
AU105977 14 50 9 AU105977 19.6 1.1 50 9 AU105977  
AU107832 15 50 9 AU107832 19.6 1.1 50 9 AU107832  
C01080 16 50 14 C01080 19.6 1.1 50 14 C01080  
AG024509 17 50 17 AG024509 19.6 1.1 50 17 AG024509  
AZ491349 18 50 17 AZ491349 19.6 1.1 40 17 AZ491349  
BH896737 19 50 17 BH896737 19.6 1.1 48 17 BH896737  
AI687542 20 50 9 AI687542 19.6 1.1 49 9 AI687542  
H41313 21 34 14 H41313 19.2 1.1 34 14 H41313  
BF211603 22 37 12 BF211603 19.2 1.1 37 12 BF211603  
BH864137 23 47 17 BH864137 19.2 1.1 47 17 BH864137  
AU102327 24 50 9 AU102327 19.2 1.1 50 9 AU102327  
AU105236 25 50 9 AU105236 19.2 1.1 50 9 AU105236  
AL756150 26 41 17 AL756150 19.2 1.1 41 17 AL756150  
AL756150 27 42 17 AL756150 19.2 1.1 42 17 AL756150  
AU102282 28 50 9 AU102282 19.2 1.1 50 9 AU102282  
AU105218 29 50 9 AU105218 19.2 1.1 50 9 AU105218  
BI102544 30 45 13 BI102544 18.8 1.1 45 13 BI102544  
BF032107 31 48 12 BF032107 18.8 1.1 48 12 BF032107  
AZ510557 32 48 17 AZ510557 18.8 1.1 48 17 AZ510557  
AU102668 33 50 9 AU102668 18.8 1.1 50 9 AU102668  
BQ704909 34 46 14 BQ704909 18.6 1.1 46 14 BQ704909  
BF722018 35 49 12 BF722018 18.6 1.1 49 12 BF722018  
AU104828 36 50 9 AU104828 18.6 1.1 50 9 AU104828  
AU107833 37 50 9 AU107833 18.6 1.1 50 9 AU107833  
AZ506007 38 40 17 AZ506007 18.4 1.1 40 17 AZ506007  
TA115C11P 39 40 17 TA115C11P 18.4 1.1 40 17 TA115C11P  
AZ463683 40 41 17 AZ463683 18.4 1.1 41 17 AZ463683  
AZ401452 41 42 17 AZ401452 18.4 1.1 42 17 AZ401452  
BH000259 42 44 17 BH000259 18.4 1.1 44 17 BH000259  
BE738342 43 45 12 BE738342 18.4 1.1 45 12 BE738342  
AI784970 44 46 9 AI784970 18.4 1.1 46 9 AI784970  
AU106899 45 50 9 AU106899 18.4 1.1 50 9 AU106899

## ALIGNMENTS

AA472672 43 bp mRNA linear EST 18-JUN-1997  
VH04G03.r1 Soares\_mammary\_gland\_NbMMG Mus musculus CDNA clone  
IMAGE:874516 5', similar to SW:NDPM\_BOVIN P42029 NADH-UBIQUINONE  
OXIDOREDUCTASE 19 KD SUBUNIT ;, mRNA sequence.  
AA472672 GI:2200954  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 43)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the

```

FEATURES             Location/Qualifiers
     1..50
        /organism="Mus musculus"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGCLM0145E01"
        /clone_lib="Mouse 10kb plasmid UUGCLM library"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /note="Vector: pW042nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydronamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pW042 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT          16 a   10 c   13 g   11 t
ORIGIN
Query Match       1-2%; Score 20.8; DB 17; Length 50;
Best Local Similarity 70.0%; Pred.No. 2.3e+05;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1652 TTCTGTGACCAACTCTTTGCCAAGAAGGCAGTGGAGAAG 1691
      ||||| |||| | ||||| ||||| ||||| ||||| |||||
Db  9 TTCTGTGACAAATCATGACCACGAAGAAGCAAGTTGGGAG 48

RESULT 3
A2785734 LOCUS
DEFINITION
ACCESSION A2785734
VERSION
KEYWORDS GSS.
SOURCE Mus musculus.
ORGANISM Mus musculus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,K., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0029 row: I column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
```



(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 9 a 7 c 14 g 6 t  
ORIGIN

Query Match 1.2%; Score 20.2; DB 17; Length 36;  
Best Local Similarity 75.8%; Pred. No. 2.9e+05;  
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 873 CTGGACACACGACGACGAGCTCTGGAG 905

Db 1 CTGGGACACCAACGGGGGATGATCTCTGGAG 33

## RESULT 6

A2391814/c

LOCUS A2391814 43 bp DNA linear GSS 03-OCT-2000  
DEFINITION IM0154H1LF Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUGC1M0154H11 F, DNA sequence.

ACCESSION A2391814

VERSION A2391814.1 GI:10506886

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 43)  
AUTHORS Dunn.D., Aoyagi.A., Barber.M., Beacorn.T., Duval.B., Hamil.C., Islam.H., Longacre.S., Mahmoud.M., Meenen.E., Pedersen.T., Reilly.M., Rose.M., Rose.R., Stokes.R., Tingey.A., von Niederhausern.A. and Wright.D., Weiss.R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0154 row: H column: 11

Seq primer: CGTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 43.

Location/Qualifiers

1. .43

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0154H11"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: pWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

## FEATURES

source

1. .49

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1154801"

/clone\_lib="NCI\_CGAP\_Ov6"

/sex="female"

/tissue\_type="normal cortical stroma"

/lab\_host="DH10B"

/note="Organ: ovary; Vector: pAMP10; mRNA made from normal

ovarian cortical stroma, cDNA made by oligo-dT priming.

Non-directionally cloned. Size-selected on agarose gel,

average insert size 600 bp.

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114[gblAF129072.1]), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT 13 a 8 c 7 g 15 t  
ORIGIN

Query Match 1.2%; Score 20.2; DB 17; Length 43;

Best Local Similarity 75.8%; Pred. No. 3.2e+05;

Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1624 CCCAGACCTGAAGACACAAAGTAGCTTCTTCT 1656

Db 38 CCCAGAACTGGACTGCAAGAAATGAGCTTTAT 6

## RESULT 7

AA627247

LOCUS AA627247

DEFINITION AA627247

ACCESSION AA627247

VERSION AA627247.1 GI:2540291

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 49)

AUTHORS NCI-CGAP

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgaps@email.nih.gov](mailto:cgaps@email.nih.gov)

Tissue Procurement: Andrew Berchuck, M.D., Elise Kohn, M.D.,

Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.lnl.gov/bbrp/image/image.html](http://www-bio.lnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 423 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1. .49

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:1154801"

/clone\_lib="NCI\_CGAP\_Ov6"

/sex="female"

/tissue\_type="normal cortical stroma"

/lab\_host="DH10B"

/note="Organ: ovary; Vector: pAMP10; mRNA made from normal

ovarian cortical stroma, cDNA made by oligo-dT priming.

Non-directionally cloned. Size-selected on agarose gel,

average insert size 600 bp.

```

BASE COUNT      13 a      8 c      22 g      6 t
ORIGIN
Query Match      1.2%; Score 20.2; DB 9; Length 49;
Best Local Similarity 68.3%; Pred. No. 3.5e+05;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 452 GGTGGTGGCGGATCAACCTATGATGGCGGCGCCCTTGCTG 492
Db 4 GGAGTTGAGGACGAGGAGCTGAGGCGCTGGCCCTAGCAG 44

RESULT 8
AW246898/c
LOCUS
DEFINITION      2822473.5prme NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822473 5',
mRNA sequence.
ACCESSION      AW246898
VERSION        AW246898.1 GI:6599891
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Other_ESTs: 2822473.3prme
Contact: Robert Strausberg, ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC Clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 19
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 49 contiguous distinct
peaks following vector sequence. Short Insert: Based upon the
presence of vector at both ends of the untrimmed sequence, this
plate probably contains a cDNA insert of approximately 464 bases.
Plate: LLC99 row: 1 column: 2
High quality sequence stop: 19.
Location/Qualifiers
1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2822473"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

* BASE COUNT      21 a      6 c      18 g      4 t
ORIGIN
```

```

Query Match      1.2%; Score 20; DB 10; Length 49;
Best Local Similarity 65.9%; Pred. No. 4.1e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

```

QY 703 TTCTGTTTGTCTCCATTCGCCCAAGAACCTCTTCACCGGGCC 746
Db 44 TTTTTCCTTTCGCCCCCTTCACCACAAAGCTTTTTCCTCGTGCC 1

RESULT 9
AU105489
LOCUS
DEFINITION      AU105489 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
COLF0946, mRNA sequence.
ACCESSION      AU105489
VERSION        AU105489.1 GI:13555010
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT        Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF0946"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT      15 a      11 c      17 g
ORIGIN

Query Match      1.2%; Score 20; DB 9; Length 50;
Best Local Similarity 65.9%; Pred. No. 4.1e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 557 AGGGATGAACACAGCGGGGAACTGGGTGTCACCTGGACACAG 600
Db 1 AGAGGATCCAGACGCGCTTGGAGGACTTGGAGCACCTGTACACAG 44

RESULT 10
AU105492
LOCUS
DEFINITION      AU105492 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC12761, mRNA sequence.
ACCESSION      AU105492
VERSION        AU105492.1 GI:13555013
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT        Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
, S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF0946"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"

BASE COUNT      15 a      11 c      17 g
ORIGIN

Query Match      1.2%; Score 20; DB 9; Length 50;
Best Local Similarity 65.9%; Pred. No. 4.1e+05;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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Db 41 TTTCTAGAGACTGTGCCACGCCGTAGTACGCCGCCGAAAG 3

RESULT 12  
AA013617

LOCUS  
DEFINITION  
AA013617  
49 bp mRNA linear EST 21-JAN-1997  
m10405.r1 Soares mouse placenta 4NDMP13.5 14.5 Mus musculus CDNA  
clone IMAGE:442089 5' similar to WP:F35G12.9 CE00978 ; , mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AA013617.1 GI:1474645  
EST.  
house mouse.  
Mus musculus

REFERENCE  
AUTHORS  
1 (bases 1 to 49)  
Marras, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

TITLE  
JOURNAL  
COMMENT  
The WashU-HMMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:267425

FEATURES  
source  
1..49  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:442089"  
/clone\_lib="Soares mouse placenta 4NDMP13.5 14.5"  
/sex="unknown"  
/tissue\_type="placenta"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)  
with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI  
1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5'  
TGTTACCAATCTGAAGTGGAGCGCCGCCGAAATTTTTTTTTTTTTTTTTTTTTTTT  
T 3'] ; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M.Fatima Bonaldo."  
7 a 13 c 15 g 14 t  
BASE COUNT  
ORIGIN

Query Match 11%; Score 19.6; DB 9; Length 49;  
Best Local Similarity 66.7%; Pred. No. 5.4e+05;  
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 605..TGCCCTGGCTGGTCCAGGACACATTGGCAGCTTTGGAGG 646  
||||| ||| ||||| ||| ||||| ||| ||||| ||| |||  
Db 7 TGCCATCTGCAGGCTCAGGTGATGGATGCTGCTCGATG 48

RESULT 13  
AA894674



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LOCUS      AA894674          49 bp      mRNA      linear      EST 09-JUN-1998
DEFINITION OJ27a03.s1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1493356 3',
            similar to SW:SPCO_HUMAN Q01082 SPECTRIN BETA CHAIN, BRAIN ;, mRNA
            sequence.
ACCESSION  AA894674
VERSION    AA894674.1 GI:3031075
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 49)
AUTHORS   Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
TITLE     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
MEDLINE   Tumor Gene Index
COMMENT    Unpublished (1997)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapb-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Sequencing by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1272 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
            Location/Qualifiers
            1..49
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:1493356"
            /clone_lib="NCI_CGAP_Kid3"
            /lab_host="DH10B"
            /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
            a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer,
            double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not
            I and Eco RI sites of the modified pT7T3 vector. mRNA
            source: 2 pooled kidneys. Library went through one round
            of normalization. Library constructed by Bento Soares and
            M. Fatima Bonaldo."
            13 a 13 c 16 g 7 t
BASE COUNT 13 a 13 c 16 g 7 t
ORIGIN
Query Match 1.1%; Score 19.6; DB 9; Length 49;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 572 CCGGGGACCTGGGTGCTGACCTGGACCGAGTGGCTGCGCCCTGCG 613
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+ Db 1 CCGGAGCAGTGGGGACCTAGACAGCTCTTCCGCTTCG 42

RESULT 14
AUI05977
LOCUS      AUI05977          50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            sequence.
ACCESSION  AUI05977
VERSION    AUI05977.1 GI:13555498
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE   mapping of mRNA start sites
COMMENT    Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@iems.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
            Location/Qualifiers
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            /db_xref="taxon:9606"
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            /clone_lib="Sugano Homo sapiens cDNA library"
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BASE COUNT 10 a 17 c 11 g 12 t
ORIGIN
Query Match 1.1%; Score 19.6; DB 9; Length 50;
Best Local Similarity 73.5%; Pred. No. 5.5e+05;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 868 ACTGCTCGCAGAGGAGCGGAGGAGGAGCTCTT 901
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Db 4 ACTCCTCGGACTCGAGACTCAGAGCTGCTCTT 37

RESULT 15
AUI07832
LOCUS      AUI07832          50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
            sequence.
ACCESSION  AUI07832
VERSION    AUI07832.1 GI:13557354
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 50)
AUTHORS   Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
TITLE     Diverse transcriptional initiation revealed by fine, large-scale
JOURNAL   EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE   mapping of mRNA start sites
COMMENT    Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@iems.u-tokyo.ac.jp
            Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
            S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
            Location/Qualifiers

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            /db_xref="taxon:9606"
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            /clone_lib="Sugano Homo sapiens cDNA library"
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            dimethylfumurate treated U937 cells"
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ORIGIN
Query Match      1.1%; Score 19.6; DB 9; Length 50;
Best Local Similarity 71.4%; Pred. No. 5.5e+05;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 433 TCCACGGAGGGGCTGATGGTGGTGGCGGCATCA 467
      ||| ||| | ||| ||| ||| ||| ||| |||
Db 3 TCCCGGCTGANGCTGGCGGTGCTGGCGGCTCA 37

Search completed: May 21, 2003, 06:14:38
Job time : 2276 secs
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